

EXHIBIT 5



Enter Text Here

All Databases

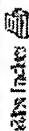
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Scores Table

Alignment

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Colours

Results of search

Number of sequences

2

Alignment score

2654

Sequence format

Pearson

Sequence type

nt

ClustalW version

1.83

Jalview

[Start Jalview](#)

Output file

[clustalw-20070522-16041749.output](#)

Alignment file

[clustalw-20070522-16041749.aln](#)

Guide tree file

[clustalw-20070522-16041749.dnd](#)

Your input file

[clustalw-20070522-16041749.input](#)

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To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the Jalview button, reload the page and check your browser settings to enable Java Applets.

Scores Table

[View Output File](#)

SeqA Name	Len (nt)	SeqB Name	Len (nt)	Score
=====	=====	=====	=====	=====
1 U25391	715	2 SEQIDNO1	1260	23.7762
2 SEQIDNO1	1260	2 SEQIDNO1	1260	53.254
=====	=====	=====	=====	=====

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

[View Output File](#)

Alignment

[Show Colors](#)[View Alignment File](#)

CLUSTAL W (1.83) multiple sequence alignment

```
U25391      TTCTTTCAATGGGAAGCAGATTGGGTACCACCCCAAGTATTGACTACCCCATCAACAAC 60
SEQIDNO1    -----

U25391      GCTATGTAATTCGTACATTACTGCCAGCCACCATGAATATTGTACGGTACCATAAATACT 120
SEQIDNO1    -----

U25391      TGACCACCTGTAGTACATAAAACCCAATCCACATCAANNCCCCCCCCCATGCTTACAA 180
SEQIDNO1    -----

U25391      GCAAGTACAGCAACCAACCCCTCAACTATCACACATCAACTGCAGCTCCAAAGCCACCTCT 240
SEQIDNO1    -----

U25391      CACCACCTAGGATACCACAACCAACCTACCCACCCTTAACAGTACATAGTACATAAAGCCAT 300
SEQIDNO1    -----

U25391      TTACCGTACATAGCACATTACAGTCAAAATCCCTTCTGTCGCCCATGGATGACCCCTCG 360
SEQIDNO1    -----GATCAGAGTCTATCACCCCTATTAACTACG 34
          *** * * * *
          * * * * *

U25391      G-AGTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTGTGCACGGGATAGCATTCGGAG 419
SEQIDNO1    GGAGCTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTGTGCACGGGATAGCATTCGGAG 94
          * *****
          * *****

U25391      ACGTGGAGCCGGAGCACCCCTATGTGCGAGTATCTGTCTTGATTCTGCCCCATCCTAT 479
SEQIDNO1    ACGTGGAGCCGGAGCACCCCTATGTGCGAGTATCTGTCTTGATTCTGCCCCATCCTAT 154
          * *****
          * *****

U25391      TATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTACTAAAGTGTGTTAATA 539
SEQIDNO1    TATTTATCGCACCTACGTTCAATATTACAGGCGAACAATACTTACTAAAGTGTGTTAATA 214
          * *****
          * *****

U25391      ATTAATGCTTGTAGGACATAATAAACAATTGAATGTGTGCACAGCCGCTTCCACACA 599
SEQIDNO1    ATTAATGCTTGTAGGACATAATAAACAATTGAATGTGTGCACAGCCGCTTCCACACA 274
          * *****
          * *****

U25391      GACATCAACAAAAAATTCACCAAAACCCCTCCCGCCGCTTCTGGCCACAGCATT 659
SEQIDNO1    GACATCAACAAAAAATTCACCAAAACCCCTCCCGCCGCTTCTGGCCACAGCATT 334
          * *****
          * *****

U25391      AAACACATCTCTGCCAAACCCCAAAACAAGAACCCCTAACACCGCTAGCCAGA---- 715
SEQIDNO1    AAACACATCTCTGCCAAACCCCAAAACAAGAACCCCTAACACCGCTAACCCAGATTTC 394
          * *****
          * *****
```

```
U25391
SEQIDNO1
-----
AAATTTTATCTTTTGGCGTATGCACCTTTTAACAGTCACCCCCCAACTAACACATTATTT 454

U25391
SEQIDNO1
-----
TCCCTCCCACTCCCATACTACTATCTCATCAATACAAACCCCGCCCATCTTACCCAGC 514

U25391
SEQIDNO1
-----
ACACACACCGCTGCTAACCCCATACCCCGGAACCAACCAACCCCAAGACACCCCCCA 574

U25391
SEQIDNO1
-----
CAGTTTATGTAGCTTACCTCCTCAAAGCAATACACTGAAAAATGTTAGACGGGCTCACAT 634

U25391
SEQIDNO1
-----
CACCCCATAAACAAATAGGTTTGGTCCTAGCCTTTCATTAGCTCTTAGTAAGATTACAC 694

U25391
SEQIDNO1
-----
ATGCAAGCATCCCCGTTCCAGTGAGTTCACCCCTCTAAATCACCACGATCAAAAGGAACAA 754

U25391
SEQIDNO1
-----
GCATCAAGCACGCAGCAATGCAGTCAAAACGCTTAGCCTAGCCACACCCCCACGGGAAA 814

U25391
SEQIDNO1
-----
CAGCAGTGATTAAACCTTTAGCAATAAACGAAAGTTTAACTAAGCTATATACTAACCCAGGG 874

U25391
SEQIDNO1
-----
TTGGTCAATTTTCGTGCCAGCCACC CGGGTCACACGATTAAACCCCAAGTCAATAGAGCCGG 934

U25391
SEQIDNO1
-----
CGTAAAGAGTGTTTTAGATCACCCCTCCCAATAAAGCTAAAACTCACCTGAGTTGTAA 994

U25391
SEQIDNO1
-----
AAACTCCAGTTGACACAAAAATAGACTACGAAAGTGGCTTTAACATACTGAAACACACAA 1054

U25391
SEQIDNO1
-----
TAGCTAAGACCCAAACTGCTGCCCAGAACACTACGAGCCACAGCTTAGCCCTAAACCTCAACAGT 1114

U25391
SEQIDNO1
-----
TAAATCAACAAAAACTGCTGCCCAGAACACTACGAGCCACAGCTTAAAACTCAAAGGACCT 1174

U25391
SEQIDNO1
-----
GGCGGTGCTTCATATCCCTCTAGAGAGCGCTTCTGTGAATCGATAAACCCCGATCAACC 1234
```

U25391 -----

SEQIDNO1 TCACCACCTCTTGCTCAGCCTATATA 1260

PLEASE NOTE: Showing colors on large alignments is slow.

[Show Colors](#) [View Alignment File](#)

Guide Tree

[Show as Phylogram Tree](#) [Show Distances](#) [View DND File](#)

(U25391:0.38112, SEQIDNO1:0.38112) ;

Cladogram

U25391
SEQIDNO1

[Show as Phylogram Tree](#) [Show Distances](#) [View DND File](#)

Right-click on the above tree to see display options.
Problems printing? Read how to print a *Phylogram* or *Cladogram*.

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